



IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

Applicants: David Duhl et al.

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For: **HUMAN CHROMOSOME 16 PLASMOLIPIN-LIKE POLYPEPTIDE**

Examiner: Sandra Wegert

Art Unit: 1642

Docket: PP-01568.002/59516-159

Date: November 4, 2002

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Commissioner for Patents
Washington, DC 20231

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STATEMENT UNDER 37 C.F.R. §1.821

Sir:

I hereby state that the content of the paper and computer-readable copies of the Sequence Listing, submitted in accordance with 37 C.F.R. §1.821, are the same.

Respectfully submitted,

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Registration No. 47,309

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Untitled.ST25.txt
SEQUENCE LISTING

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<110> Duhl, David
Gorman, Susan W

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<130> PP-01568.002/59516-159

<140> US 09/602,597

<141> 2000-06-22

<160> 12

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 35 40 45

Tyr Asp Pro Arg Ser Leu Tyr Glu Arg Leu Gln Glu Gln Lys Asp Arg
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Lys Gln Gln Glu Tyr Glu Glu Gln Phe Lys Phe Lys Asn Met Val Arg
 65 70 75 80

Gly Leu Asp Glu Asp Glu Thr Asn Phe Leu Asp Glu Val Ser Arg Gln
 85 90 95

Gln Glu Leu Ile Glu Lys Gln Arg Arg Glu Glu Glu Leu Lys Glu Leu
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 115 120 125

Lys Lys Glu Val Glu Lys Lys Leu Thr Val Lys Pro Ile Glu Thr Lys
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180 185 190

Thr Ser Leu Ser Gly Pro Ser Ile His Cys Pro Ser Ala Ala Val Cys
195 200 205

Ile Gly Ile Leu Pro Gly Leu Gly Ala Tyr Ser Gly Ser Ser Asp Ser
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Leu Ile Ala Asp Thr Pro Tyr His	Leu Tyr Pro Ala Tyr Gly Trp Val		
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Leu Tyr Leu Phe Gln Leu His Met	Lys Leu Tyr Met Val Pro Trp Pro		
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Arg Gly Val Gly Ser Asn Ala Ala	Thr Ser Gln Met Ala Gly Gly Tyr		
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Arg Pro Thr Ala Leu Met Ser Ser Thr Val Ala Ala Ala Ala Pro Ala
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Ala Gly Ala Ala Ser Arg Lys Glu Ser Pro Gly Arg Trp Gly Leu Gly
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Glu Asp Pro Thr Gly Val Ser Pro Ser Leu Gln Cys Arg Val Cys Gly
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cag	gtg	ggg	gca	ggg	atg	tgc	ccc	gtg	gac	aag	gcc	cac	cgc	aac	cag	463
Gln	Val	Gly	Ala	Gly	Met	Cys	Pro	Val	Asp	Lys	Ala	His	Arg	Asn	Gln	
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Cys	Gln	Ala	Cys	Arg	Leu	Lys	Lys	Cys	Leu	Gln	Ala	Gly	Met	Asn	Gln	
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Asn Gly Cys Thr Gly Phe Phe Lys Arg Ser Val Arg Arg Arg Leu Ile
65 70 75 80

Tyr Arg Cys Gln Val Gly Ala Gly Met Cys Pro Val Asp Lys Ala His
85 90 95

Arg Asn Gln Cys Gln Ala Cys Arg Leu Lys Lys Cys Leu Gln Ala Gly
100 105 110

Met Asn Gln Asp Ala Val Gln Lys Glu Arg Gln Pro Arg Ser Thr Ala
115 120 125

Gln Val His Leu Asp Ser Met Glu Ser Asn Thr Glu Ser Arg Pro Glu
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Ser Leu Val Ala Pro Pro Ala Pro Ala Gly Arg Ser Pro Arg Gly Pro
145 150 155 160

Thr Pro Met Ser Ala Ala Arg Ala Leu Gly His His Phe Met Ala Ser
165 170 175

Leu Ile Thr Ala Glu Thr Cys Ala Lys Leu Glu Pro Glu Asp Ala Asp
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Glu Asn Ile Asp Val Thr Ser Asn Asp Pro Glu Phe Pro Ser Ser Pro
195 200 205

Tyr Ser Ser Ser Ser Pro Cys Gly Leu Asp Ser Ile His Glu Thr Ser
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Phe Ser Ser Leu Pro Phe Arg Asp Gln Val Pro Thr Gly Leu Pro Ala
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Untitled.ST25.txt

Gly Glu Leu Gly Trp Ala Gly Val Arg Arg Pro Thr Arg Val Asn Gln
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Thr Gly His Thr His Pro His Ala Ser Met Asn Ala His Ser Leu Asp
 275 280 285

Gly Asp Gly Trp Gly His Thr Tyr Leu
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<213> Homo sapiens

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 cccagcagc gggggcagcc cccatgggcc ccagttattg cgtgtgcaag gtggagctgt 120
 cagtgagtgg ccagaacct a ctggaccggg atgttacctc caagtccgac cccttctgtg 180
 tcctctttac agagaacaat ggcagatgga tcgag 215

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<211> 3686

<212> DNA

<213> Homo sapiens

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<221> CDS

<222> (658)..(2196)

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ccgagtagct gggattacag gtggtgactt ccaagagtga ctccgtcgga ggaaaatgac 180
tccccagtcg ctgctgcaga cgacactggt cctgctgagt ctgctcttcc tggccaagc 240
cagcgggaacc agacacacag gagcagcctc cactacaaac ccacaccaga cctgcgcctc 300
tccatcgaga actccgaaga ggccctcaca gtccatgccc ctttccctgc agcccaccct 360
gcttcccgat ccttccctga cccagggggc ctctaccact tctgcctcta ctggaaccga 420
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tctagcctcc tctgcttcca gcaccaggag gagagcctgg ctccagggccc cccgctgtta 540
gccacttctg tcacctctg gtggagccct cagaacatca gcctgccag tgccgccagc 600
ttcaccttct ccttccacag tctccccac acggccgctc acaatgcctc ggtggac 657
atg tgc gag ctc aaa agg gac ctc cag ctg ctc agc cag ttc ctg aag 705
Met Cys Glu Leu Lys Arg Asp Leu Gln Leu Leu Ser Gln Phe Leu Lys
1 5 10 15
cat ccc cag aag gcc tca agg agg ccc tcg gct gcc ccc gcc agc cag 753
His Pro Gln Lys Ala Ser Arg Arg Pro Ser Ala Ala Pro Ala Ser Gln
20 25 30
cag ttg cag agc ctg gag tcg aaa ctg acc tct gtg aga ttc atg ggg 801
Gln Leu Gln Ser Leu Glu Ser Lys Leu Thr Ser Val Arg Phe Met Gly
35 40 45
gac atg gtg tcc ttc gag gag gac cgg atc aac gcc acg gtg tgg aag 849
Asp Met Val Ser Phe Glu Glu Asp Arg Ile Asn Ala Thr Val Trp Lys
50 55 60
ctc cag ccc aca gcc ggc ctc cag gac ctg cac atc cac tcc cgg cag 897
Leu Gln Pro Thr Ala Gly Leu Gln Asp Leu His Ile His Ser Arg Gln
65 70 75 80
gag gag gag cag agc gag atc atg gag tac tcg gtg ctg ctg cct cga 945
Glu Glu Glu Gln Ser Glu Ile Met Glu Tyr Ser Val Leu Leu Pro Arg
85 90 95
aca ctc ttc cag agg acg aaa ggc cgg agg ggg gag gct gag aag aga 993
Thr Leu Phe Gln Arg Thr Lys Gly Arg Arg Gly Glu Ala Glu Lys Arg
100 105 110
ctc ctc ctg gtg gac ttc agc agc caa gcc ctg ttc cag gac aag aat 1041
Leu Leu Leu Val Asp Phe Ser Ser Gln Ala Leu Phe Gln Asp Lys Asn
115 120 125

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Untitled.ST25.txt

tcc agc cac gtc ctg ggt gag aag gtc ttg ggg att gtg gta cag aac Ser Ser His Val Leu Gly Glu Lys Val Leu Gly Ile Val Val Gln Asn 130 135 140	1089
acc aaa gta gcc aac ctc acg gag ccc gtg gtg ctc acc ttc cag cac Thr Lys Val Ala Asn Leu Thr Glu Pro Val Val Leu Thr Phe Gln His 145 150 155 160	1137
cag cta cag ccg aag aat gtg act ctg caa tgt gtg ttc tgg gtt gaa Gln Leu Gln Pro Lys Asn Val Thr Leu Gln Cys Val Phe Trp Val Glu 165 170 175	1185
gac ccc aca ttg agc agc ccg ggg cat tgg agc agt gct ggg tgt gag Asp Pro Thr Leu Ser Ser Pro Gly His Trp Ser Ser Ala Gly Cys Glu 180 185 190	1233
acc gtc agg aga gaa acc caa aca tcc tgc ttc tgc aac cac ttg acc Thr Val Arg Arg Glu Thr Gln Thr Ser Cys Phe Cys Asn His Leu Thr 195 200 205	1281
tac ttt gca gtg ctg atg gtc tcc tgc gtg gag gtg gac gcc gtg cac Tyr Phe Ala Val Leu Met Val Ser Ser Val Glu Val Asp Ala Val His 210 215 220	1329
aag cac tac ctg agc ctc ctc tcc tac gtg ggc tgt gtc gtc tct gcc Lys His Tyr Leu Ser Leu Leu Ser Tyr Val Gly Cys Val Val Ser Ala 225 230 235 240	1377
ctg gcc tgc ctt gtc acc att gcc gcc tac ctc tgc tcc agg agg aaa Leu Ala Cys Leu Val Thr Ile Ala Ala Tyr Leu Cys Ser Arg Arg Lys 245 250 255	1425
cct cgg gac tac acc atc aag gtg cac atg aac ctg ctg ctg gcc gtc Pro Arg Asp Tyr Thr Ile Lys Val His Met Asn Leu Leu Leu Ala Val 260 265 270	1473
ttc ctg ctg gac acg agc ttc ctg ctc agc gag ccg gtg gcc ctg aca Phe Leu Leu Asp Thr Ser Phe Leu Leu Ser Glu Pro Val Ala Leu Thr 275 280 285	1521
ggc tct gag gct ggc tgc cga gcc agt gcc atc ttc ctg cac ttc tcc Gly Ser Glu Ala Gly Cys Arg Ala Ser Ala Ile Phe Leu His Phe Ser 290 295 300	1569
ctg ctc acc tgc ctt tcc tgg atg ggc ctc gag ggg tac aac ctc tac Leu Leu Thr Cys Leu Ser Trp Met Gly Leu Glu Gly Tyr Asn Leu Tyr 305 310 315 320	1617
cga ctc gtg gtg gag gtc ttt ggc acc tat gtc cct ggc tac cta ctc Arg Leu Val Val Glu Val Phe Gly Thr Tyr Val Pro Gly Tyr Leu Leu 325 330 335	1665
aag ctg agc gcc atg ggc tgg ggc ttc ccc atc ttt ctg gtg acg ctg Lys Leu Ser Ala Met Gly Trp Gly Phe Pro Ile Phe Leu Val Thr Leu 340 345 350	1713
gtg gcc ctg gtg gat gtg gac aac tat ggc ccc atc atc ttg gct gtg Val Ala Leu Val Asp Val Asp Asn Tyr Gly Pro Ile Ile Leu Ala Val 355 360 365	1761

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cat agg act cca gag ggc gtc atc tac cct tcc atg tgc tgg atc cgg His Arg Thr Pro Glu Gly Val Ile Tyr Pro Ser Met Cys Trp Ile Arg 370 375 380	1809
gac tcc ctg gtc agc tac atc acc aac ctg ggc ctc ttc agc ctg gtg Asp Ser Leu Val Ser Tyr Ile Thr Asn Leu Gly Leu Phe Ser Leu Val 385 390 395 400	1857
ttt ctg ttc aac atg gcc atg cta gcc acc atg gtg gtg cag atc ctg Phe Leu Phe Asn Met Ala Met Leu Ala Thr Met Val Val Gln Ile Leu 405 410 415	1905
cgg ctg cgc ccc cac acc caa aag tgg tca cat gtg ctg aca ctg ctg Arg Leu Arg Pro His Thr Gln Lys Trp Ser His Val Leu Thr Leu Leu 420 425 430	1953
ggc ctc agc ctg gtc ctt ggc ctg ccc tgg gcc ttg atc ttc ttc tcc Gly Leu Ser Leu Val Leu Gly Leu Pro Trp Ala Leu Ile Phe Phe Ser 435 440 445	2001
ttt gct tct ggc acc ttc cag ctt gtc gtc ctc tac ctt ttc agc atc Phe Ala Ser Gly Thr Phe Gln Leu Val Val Leu Tyr Leu Phe Ser Ile 450 455 460	2049
atc acc tcc ttc caa ggc ttc ctc atc ttc atc tgg tac tgg tcc atg Ile Thr Ser Phe Gln Gly Phe Leu Ile Phe Ile Trp Tyr Trp Ser Met 465 470 475 480	2097
cgg ctg cag gcc cgg ggt ggc ccc tcc cct ctg aag agc aac tca gac Arg Leu Gln Ala Arg Gly Gly Pro Ser Pro Leu Lys Ser Asn Ser Asp 485 490 495	2145
agc gcc agg ctc ccc atc agc tcg ggc agc acc tcg tcc agc cgc atc Ser Ala Arg Leu Pro Ile Ser Ser Gly Ser Thr Ser Ser Arg Ile 500 505 510	2193
tag gcctccagcc cacctgccca tgtgatgaag cagagatgcg gcctcgtcgc	2246
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Untitled.ST25.txt

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<212> PRT

<213> Homo sapiens

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Met Cys Glu Leu Lys Arg Asp Leu Gln Leu Leu Ser Gln Phe Leu Lys
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His Pro Gln Lys Ala Ser Arg Arg Pro Ser Ala Ala Pro Ala Ser Gln
20           25           30

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Gln Leu Gln Ser Leu Glu Ser Lys Leu Thr Ser Val Arg Phe Met Gly
35           40           45

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Asp Met Val Ser Phe Glu Glu Asp Arg Ile Asn Ala Thr Val Trp Lys
50           55           60

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Leu Gln Pro Thr Ala Gly Leu Gln Asp Leu His Ile His Ser Arg Gln
65           70           75           80

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Untitled.ST25.txt

Glu Glu Glu Gln Ser Glu Ile Met Glu Tyr Ser Val Leu Leu Pro Arg
85 90 95

Thr Leu Phe Gln Arg Thr Lys Gly Arg Arg Gly Glu Ala Glu Lys Arg
100 105 110

Leu Leu Leu Val Asp Phe Ser Ser Gln Ala Leu Phe Gln Asp Lys Asn
115 120 125

Ser Ser His Val Leu Gly Glu Lys Val Leu Gly Ile Val Val Gln Asn
130 135 140

Thr Lys Val Ala Asn Leu Thr Glu Pro Val Val Leu Thr Phe Gln His
145 150 155 160

Gln Leu Gln Pro Lys Asn Val Thr Leu Gln Cys Val Phe Trp Val Glu
165 170 175

Asp Pro Thr Leu Ser Ser Pro Gly His Trp Ser Ser Ala Gly Cys Glu
180 185 190

Thr Val Arg Arg Glu Thr Gln Thr Ser Cys Phe Cys Asn His Leu Thr
195 200 205

Tyr Phe Ala Val Leu Met Val Ser Ser Val Glu Val Asp Ala Val His
210 215 220

Lys His Tyr Leu Ser Leu Leu Ser Tyr Val Gly Cys Val Val Ser Ala
225 230 235 240

Leu Ala Cys Leu Val Thr Ile Ala Ala Tyr Leu Cys Ser Arg Arg Lys
245 250 255

Pro Arg Asp Tyr Thr Ile Lys Val His Met Asn Leu Leu Leu Ala Val
260 265 270

Phe Leu Leu Asp Thr Ser Phe Leu Leu Ser Glu Pro Val Ala Leu Thr
275 280 285

Gly Ser Glu Ala Gly Cys Arg Ala Ser Ala Ile Phe Leu His Phe Ser
290 295 300

Leu Leu Thr Cys Leu Ser Trp Met Gly Leu Glu Gly Tyr Asn Leu Tyr

305		310		315		320									
Arg	Leu	Val	Val	Glu	Val	Phe	Gly	Thr	Tyr	Val	Pro	Gly	Tyr	Leu	Leu
				325					330					335	
Lys	Leu	Ser	Ala	Met	Gly	Trp	Gly	Phe	Pro	Ile	Phe	Leu	Val	Thr	Leu
			340					345					350		
Val	Ala	Leu	Val	Asp	Val	Asp	Asn	Tyr	Gly	Pro	Ile	Ile	Leu	Ala	Val
		355					360					365			
His	Arg	Thr	Pro	Glu	Gly	Val	Ile	Tyr	Pro	Ser	Met	Cys	Trp	Ile	Arg
	370					375					380				
Asp	Ser	Leu	Val	Ser	Tyr	Ile	Thr	Asn	Leu	Gly	Leu	Phe	Ser	Leu	Val
385					390					395					400
Phe	Leu	Phe	Asn	Met	Ala	Met	Leu	Ala	Thr	Met	Val	Val	Gln	Ile	Leu
			405						410					415	
Arg	Leu	Arg	Pro	His	Thr	Gln	Lys	Trp	Ser	His	Val	Leu	Thr	Leu	Leu
			420					425					430		
Gly	Leu	Ser	Leu	Val	Leu	Gly	Leu	Pro	Trp	Ala	Leu	Ile	Phe	Phe	Ser
		435					440					445			
Phe	Ala	Ser	Gly	Thr	Phe	Gln	Leu	Val	Val	Leu	Tyr	Leu	Phe	Ser	Ile
	450					455					460				
Ile	Thr	Ser	Phe	Gln	Gly	Phe	Leu	Ile	Phe	Ile	Trp	Tyr	Trp	Ser	Met
465					470					475					480
Arg	Leu	Gln	Ala	Arg	Gly	Gly	Pro	Ser	Pro	Leu	Lys	Ser	Asn	Ser	Asp
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<213> Homo sapiens

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<211> 5

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<210> 12

<211> 10

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Ser Ala Trp Arg His Pro Gln Phe Gly Gly
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